25R 5'-AAC GAC GTC TGG TGC GTG-3' (SEQ ID NO:59)

33 5'-TGC AGC TAT ATG ACC TTC CCC CTC-3' (SEQ ID NO:60)

D1 cont.

37 5'-GGA CAT GCT GAT GGC TCA GA-3' (SEQ ID NO:61)

38 5'-CAG AAC TTG TCT CAT CCC TG-3 (SEQ ID NO:62)

38A 5'-GGC TAT ACA TTG GGA CTA ACA-3' (SEQ ID NO:63)

38B 5'-CGA ATC ATC ACA TCC TAT GTT-3' (SEQ ID NO:64)

39 5'-GCA AGT TCG ACT TCC AC-3' (SEQ ID NO:65)

39A 5'-TCG ACT TCC ACA AGT ACA TCA-3' (SEQ ID NO:66)

53 5'-AGC GTA CCT GCG TAC GTA G-3' (SEQ ID NO:67)

Please replace the paragraph beginning at page 30, line 21, with the following rewritten paragraph:

By way of example for nucleic acid testing, the barley *mlo-5* resistance allele is characterized by a G- to A-nucleotide substitution in the predicted start codon of the *Mlo* gene (Table 1). The mutation may easily be detected by standard PCR amplification of a *Mlo* gene segment from genomic template DNA with the primers:

D2

forward primer: 5'-GTTGCCACACTTTGCCACG-3' (SEQ ID NO:68)

reverse primer: 5'-AAGCCAAGACGACAATCAGA-3' (SEQ ID NO:69)

(for example), followed by digestion with the restriction enzyme *Psh*A1. This generates a cleaved amplified polymorphic sequences (CAPS) marker which may be displayed using conventional agarose gel electrophoresis. Presence of

a 769 bp fragment is indicative of the presence of the *mlo-5* allele.

Please replace the paragraph beginning at page 31, line 7, with the following rewritten paragraph:

The *mlo-9* resistance allele is characterized by a C- to T- nucleotide substitution (Table 1). This allele is of particular relevance since it is used frequently in breeding material. The mutational event may be easily detected using the primers:

forward primer 5'-GRRGCCACACTTTGCCACG-3' (SEQ ID NO:70)

reverse primer 5'-AAGCCAAGACGACAATCAGA-3' (SEQ ID NO:71)

(for example) and subsequent digestion of genomic amplification products with the restriction enzyme *Hha*1. This generates a CAPS marker which may be displayed by conventional agarose gel electrophoresis. The presence of a 374 bp fragment is indicative of the presence of *mlo-9*.

Page 61, line 2, insert the following heading:

--Brief Description of the Drawings--.

Please replace the paragraph beginning at page 62, line 21, with the following rewritten paragraph:

Figure 2 shows an *Mlo* coding sequence and encoded amino acid sequence according to the present invention (SEQ ID NOs:1 and 2). The amino acid sequence predicted from DNA sequences of RT-PCR products from Ingrid *Mlo* are shown. Nucleotide numbers are given according to translational start site.

D4

Please replace the paragraphs beginning at page 64, line 14, with the following rewritten paragraphs:

Figure 5 shows an alignment of genomic sequences covering the barley *Mlo* gene and a rice homologue isolated *via* crosshybridization with a barley gene specific probe (SEQ ID NOs:3 and 4). The top line shows the barley *Mlo* genomic DNA sequence (exon sequences underlined). The bottom line shows the rice genomic sequence containing the rice *Mlo* homologue.

D5

Figure 6 shows an alignment of genomic sequences carrying the barley *Mlo* gene and a barley homologue isolated *via* crosshybridization with a barley gene specific probe (SEQ ID NOs:5 and 6). The top line shows the barley

Mlo genomic DNA sequence (exon sequences underlined). The bottom line shows the genomic sequence containing the barley *Mlo* homologue.

D5 Cont.

Figure 7 Nucleotide and Deduced Amino Acid Sequence of the Barley *Mlo* cDNA (SEQ ID NOs:7 and 8). The nucleotide and the deduced amino acid sequence are based on the combined data of RT-PCR and RACE obtained from experiments using RNA of cultivar Ingrid *Mlo*. The stop codon is marked by an asterisk, the putative polyadenylation signal is underlined and the detected termini of RACE products are indicated by arrows above the sequence. Positions of introns as indentified by comparison with corresponding genomic clones are labelled by triangles below the nucleic acid sequence. Six predicted transmembrane spanning helices according to the MEMSAT algorithm (Jones *et al.*, 1994) are boxed in grey colour. A putative nuclear localization signal (K-K-K-V-R) and casein kinase II site (S-I-F-D) in the carboxy-terminal half of the protein are shown in bold type.

Please replace the paragraphs beginning at page 65 line 14, with the following rewritten paragraphs:

Figure 8 shows genomic sequence of rice (Oryza sativa) homologue including coding and flanking sequences (SEQ ID NO:9).

D5 Cont

Figure 9 shows genomic sequence of barley (Hordeum vulgare) homologue including coding and flanking sequences (SEQ ID NO:10).

Figure 10 shows cDNA sequence of rice homologue.

Figure 11 (SEQ ID NO:12) shows cDNA sequence of barley homologue (SEQ ID NO:11).

Figure 12 shows cDNA sequence of Arabidopsis thaliana homologue (SEQ ID NO:13).

Figure 13 shows amino acid sequence of rice homologue (SEQ ID NO:14).

Figure 14 shows amino acid sequence of barley homologue (SEQ ID NO:15).

Figure 15 shows amino acid sequence of Arabidopsis homologue (SEQ ID NO:16).

Figure 16 shows a pretty box of amino acid sequences of Mlo, barley, rice and Arabidopsis homologues (SEQ ID NOs:17-19).

Please replace the paragraph beginning at page 85, line 8, with the following rewritten paragraph:

A compilation of the *mlo* mutants and their mother varieties analyzed in this study has been described by Jørgensen (1992) and by Habekuss and Hentrich (1988). Since mutant 2118 has not been assigned to an allele number so far, we designate the allele here as *mlo*-26, according to current numbering in the GrainGene database (gopher colon forward slash forward slash greengenes dot cit dot cornell dot edu colon 70 forward slash 77 forward slash dot graingenes dot ndx forward slash index question mark mlo).

Please replace the paragraph beginning at page 89, line 24, with the following rewritten paragraph:

RT-PCR was performed using the SUPERSCRIPT preamplification system for first strand cDNA synthesis (Gibco BRL). Total RNA (1 µg) of seven-day-old primary barley leaves (cultivar Ingrid) served as template. First strand cDNA synthesis was primed by an oligo(dT) primer. The putative coding region of the *Mlo* gene was subsequently amplified using oligonucleotides 25L (GTGCATCTGCGTGTGCGTA) (SEQ ID NO:72) and 38 (CAGAAACTTGTCTCATCCCTG) (SEQ ID NO:73) in a single amplification step (35 cycles, 60°C

annealing temperature). The resulting product was analyzed by direct sequencing. 5'- and 3'-ends of the *Mlo* cDNA were determined by RACE (Frohman et al., 1988) using the MARATHON cDNA amplification kit (Clontech). Corresponding experimental procedures were mainly carried out according to the instructions of the manufacturer. To obtain specific RACE products, two consecutive rounds of amplification (35 cycles, 55°C annealing temperature) were necessary. For this purpose, two sets of nested primers were used in combination with the adapter primers of the kit: oligonucleotides 46 (AGGGTCAGGATCGCCAC) (SEQ ID NO:74) and 55 (TTGTGGAGGCCGTGTTCC) (SEQ ID NO:75) for the 5'-end and primers 33 (TGCAGCTATATGACCTTCCCCCTC) (SEQ ID NO:76) and 37 (GGACATGCTGATGGCTCAGA) (SEQ ID NO:77) for the 3'-end. RACE products were subcloned into pBluescript SK (Stratagene). Ten 5'-end and eight 3' end clones were chosen for DNA sequence analysis.

Please replace the paragraphs beginning at page 91, line 24, with the following rewritten paragraphs:

Table 5A show amino acid sequences, with "query" indicating part of the Mlo protein sequence to which homology has been found, with the predicted amino acid

sequence of each identified EST marked with "subject" (SEQ ID NOs:20-49).

Please replace the paragraph beginning at page 92, line 1, with the following rewritten paragraph:

Table 5B shows EST nucleotide sequences encoding the amino acid sequences shown in Table 5A (SEQ ID NOs:50-56). GenBank Accession number T22145 (definition 4153 Arabidopsis thaliana cDNA clone 97N8T7, NCBI Seq ID 932185), number T22146 (definition 4153 Arabidopsis thaliana cDNA clone 97N9T7, NCBI Seq ID 932186), number N37544 (definition 18771 Arabidopsis thaliana cDNA clone 205N12T7, NCBI Seq ID 1158686), number T88073 (definition 11769 Arabidopsis thaliana cDNA clone 155I23T7, NCBI Seq ID 935932) number H76041 (definition 17746 Arabidopsis thaliana cDNA clone 193P6T7, NCBI seq ID 1053292), number D24287 (rice cDNA partial sequence R1638_1A, nID g428139) and D24131 (rice cDNA partial sequence R1408_1A, nID g427985) are shown. The Arabidopsis sequences are from Newman *et al.* (1994) *Plant Physiol.* **106** 1241-55. The rice sequences are from Minobe, Y. and Sasaki, T. submitted 2 Nov 1993 to DDBJ.